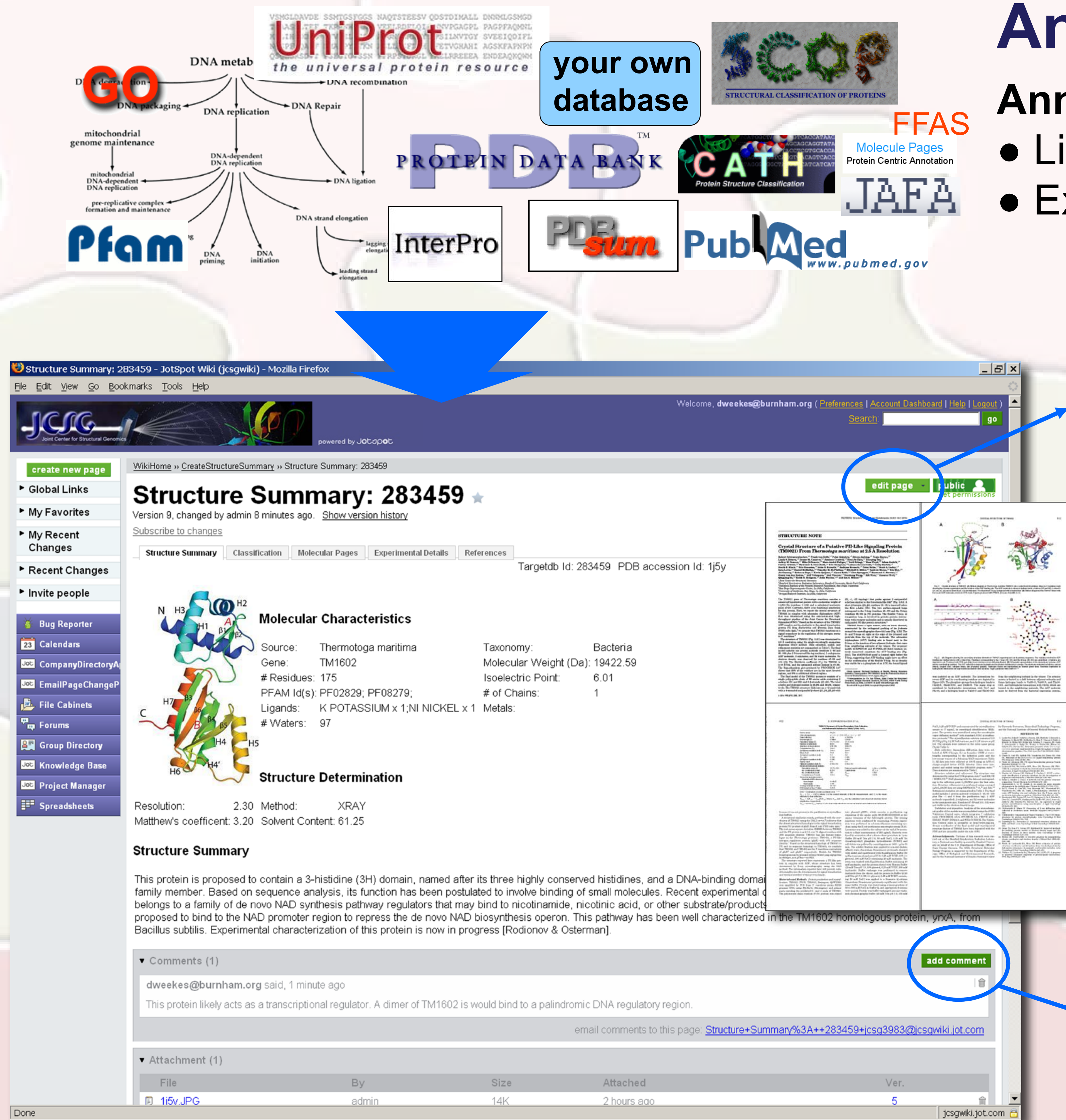
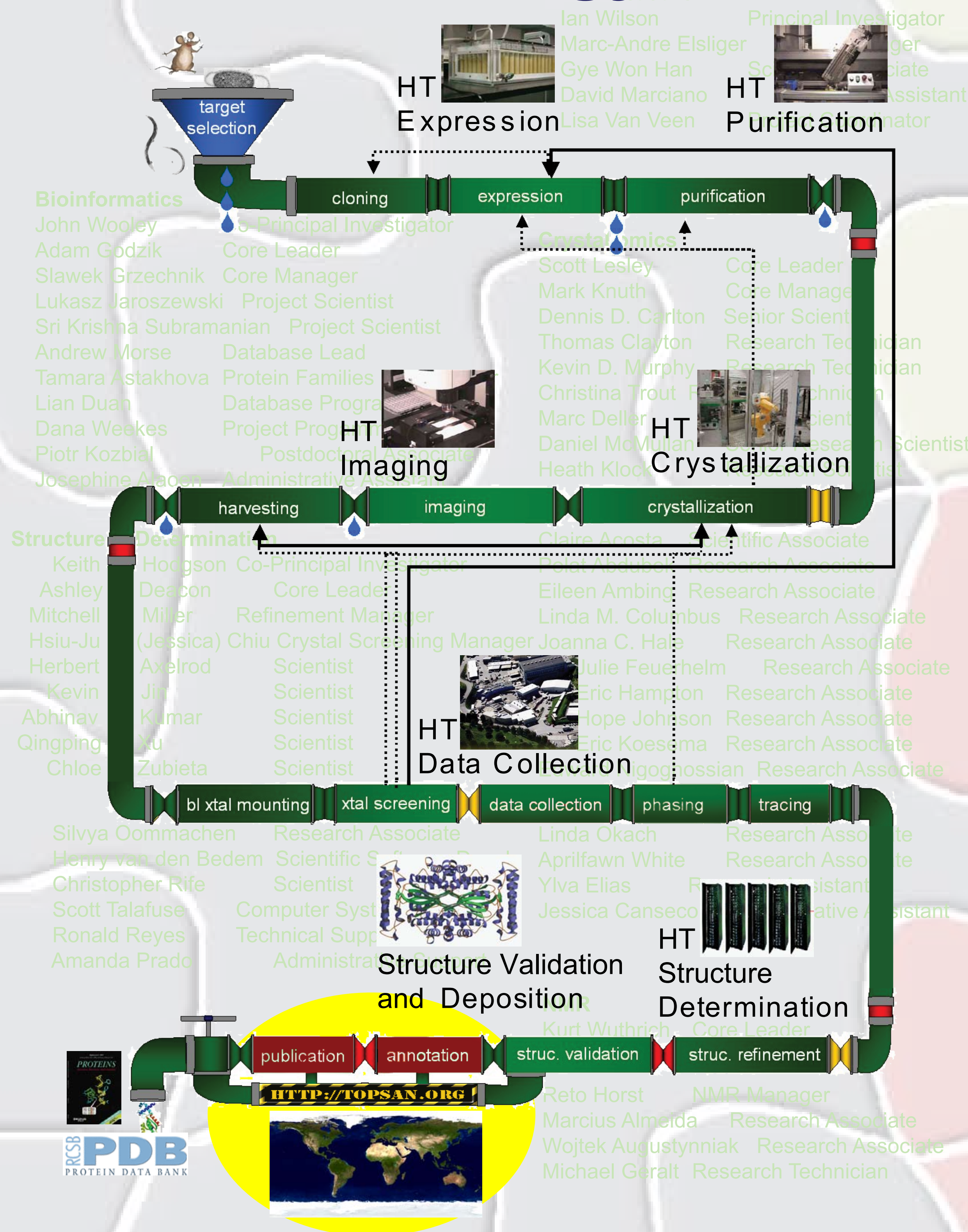


Introduction

The Joint Center for Structural Genomics (JCSG) is one of the four large-scale structural genomics centers funded by the U.S. National Institutes of Health (NIH) as part of the Protein Structure Initiative (PSI). PSI centers have determined high-resolution structures of several novel, previously uncharacterized protein families for which associated biochemical and biological research are not available. Consequently, the vast majority of these structures are not described in high impact, peer-reviewed manuscripts. Here, we propose TOPSAN, a radically novel way to collect, share and distribute information about protein three-dimensional structures.

JCSG technology pipeline



Annotating data from HT centers

Annotation:

- Live feeds from public databases
- Expert-curated information (collective intelligence)

Content management:

- Wiki-style editing
- Page-level access control
- Online WYSIWYG editor
- Email notification
- Structured fields + free text

Quality control & authorship:

- Encourage community collaboration
- JCSG scientists & invited peers
- Many authors - No contribution too small
- Lead authors (editors) in charge of releases

Publication tools:

- Instant publication of “development” versions
- Releases of polished editions of the articles
- Open for comments at any time

Perspectives

TOPSAN is a pilot project towards creating an open annotation platform that will enable us to collect, share and distribute information about proteins in the form of expert-curated annotations combined with information obtained from a network of collaborating resources, enabling us to understand the functions and roles of these proteins in their respective organisms.

Acknowledgments

Thanks to all members of the JCSG.
 Grant sponsor: National Institutes of Health, Protein Structure Initiative.
 Grant numbers: P50 GM62411, U54 GM074898

Structural Genomics of *Thermotoga maritima*

Thermotoga maritima is an extremophilic bacterium that thrives in high-temperature ecosystems. This organism, which has an exceptionally deep evolutionary connection to higher life forms, is the primary target for the high-throughput (HT) protein structure determination effort at the JCSG. By focusing HT methodology on *Thermotoga maritima*, we hope to obtain genome-wide fold coverage for this organism. Such studies will enable us to gain insights into the structural nature of complex life forms, down to the atomic level.

